



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2023 – 12:29 pm GMT

PDB ID : 2WCG
Title : X-ray structure of acid-beta-glucosidase with N-octyl(cyclic guanidine)-nojiri mycin in the active site
Authors : Brumshtein, B.; Aguilar, M.; Garcia-Moreno, M.I.; Mellet, C.O.; Garcia-Fernandez, J.M.; Silman, I.; Shaaltiel, Y.; Aviezer, D.; Sussman, J.L.; Futerman, A.H.
Deposited on : 2009-03-12
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

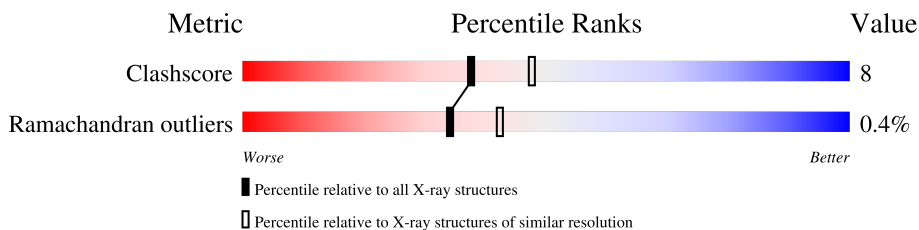
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.





Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	505	
1	B	505	
2	C	3	
2	D	3	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	C	1	-	-	X	-
2	NAG	D	1	-	-	X	-
3	FUC	B	1501	-	-	X	-

2 Entry composition [i](#)

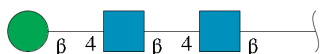
There are 7 unique types of molecules in this entry. The entry contains 8672 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GLUCOSYLCERAMIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	493	3865	2494	660	695	16	0	0	0
1	B	495	3878	2501	661	700	16	0	0	0

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	3	39	22	2	15	0	0	0
2	D	3	39	22	2	15	0	0	0

- Molecule 3 is alpha-L-fucopyranose (three-letter code: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		
3	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 4 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



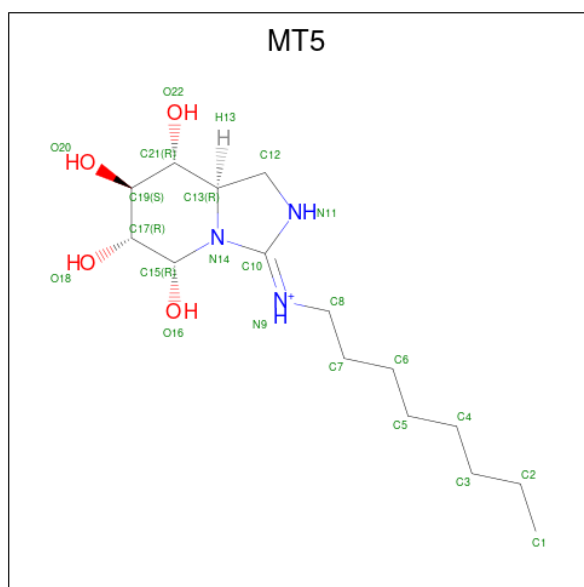
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0

- Molecule 5 is N-[(3E,5R,6R,7S,8R,8AR)-5,6,7,8-TETRAHYDROXYHEXAHYDROIMIDAZO[1,5-A]PYRIDIN-3(2H)-YLIDENE]OCTAN-1-AMINIUM (three-letter code: MT5) (formula: $C_{15}H_{30}N_3O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	7	3	4		
5	B	1	Total	C	N	O	0	0
			14	7	3	4		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		
6	B	1	Total	Cl	0	0
			1	1		

- Molecule 7 is water.

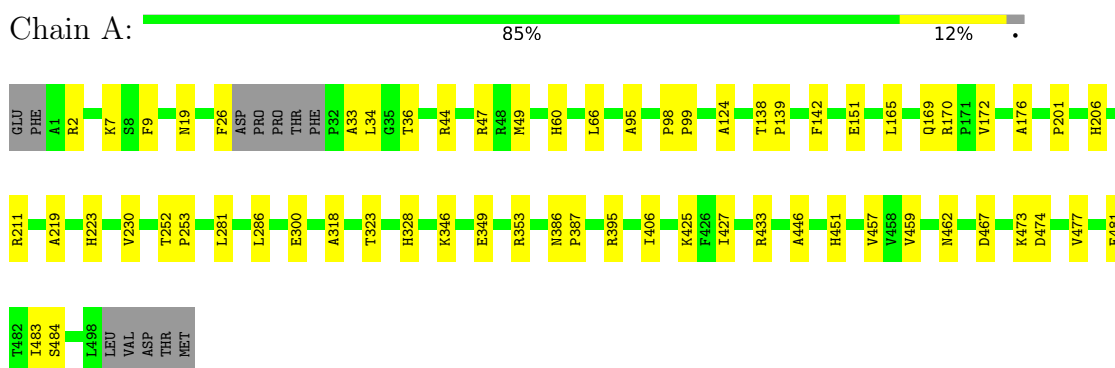
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	369	Total	O	0	0
			369	369		
7	B	372	Total	O	0	0
			372	372		

3 Residue-property plots [i](#)

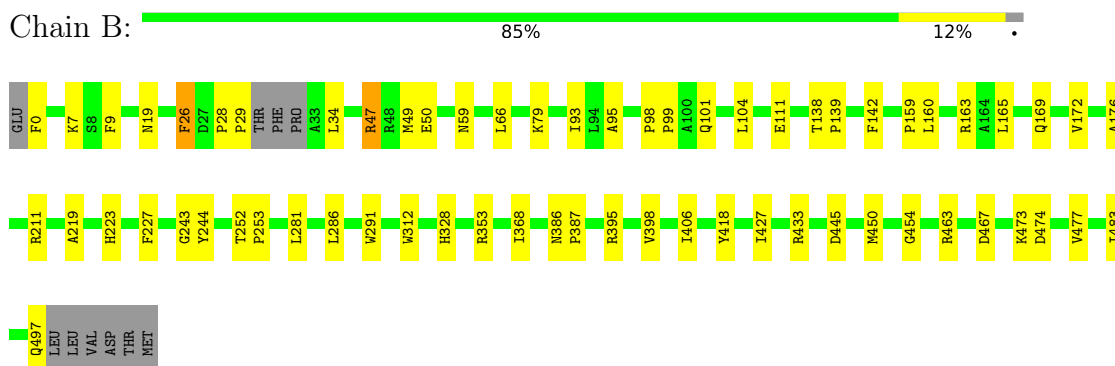
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

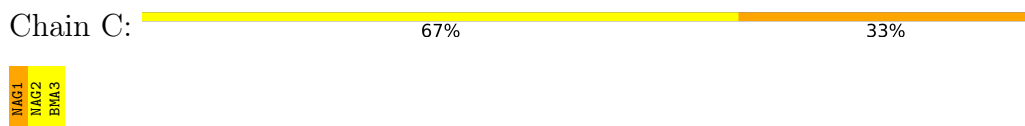
- Molecule 1: GLUCOSYLCERAMIDASE



- Molecule 1: GLUCOSYLCERAMIDASE



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2
BMA3

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.31Å 96.83Å 83.23Å 90.00° 104.34° 90.00°	Depositor
Resolution (Å)	19.74 – 2.30	Depositor
% Data completeness (in resolution range)	99.7 (19.74-2.30)	Depositor
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.4.0067	Depositor
R, R_{free}	0.135 , 0.194	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	8672	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MT5, BMA, FUC, CL, SO4, NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.90	0/3982	0.86	6/5431 (0.1%)
1	B	0.90	3/3996 (0.1%)	0.84	4/5451 (0.1%)
All	All	0.90	3/7978 (0.0%)	0.85	10/10882 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	26	PHE	CB-CG	-6.10	1.41	1.51
1	B	433	ARG	CZ-NH1	-5.40	1.26	1.33
1	B	398	VAL	CB-CG1	5.26	1.63	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	ARG	NE-CZ-NH2	-10.06	115.27	120.30
1	B	433	ARG	NE-CZ-NH2	9.18	124.89	120.30
1	A	433	ARG	NE-CZ-NH1	8.48	124.54	120.30
1	A	47	ARG	NE-CZ-NH1	8.37	124.49	120.30
1	B	353	ARG	NE-CZ-NH1	7.20	123.90	120.30
1	B	47	ARG	NE-CZ-NH1	-6.42	117.09	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	47	ARG	NE-CZ-NH2	6.12	123.36	120.30
1	A	353	ARG	NE-CZ-NH2	5.85	123.22	120.30
1	A	353	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	A	353	ARG	NH1-CZ-NH2	-5.18	113.70	119.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	34	LEU	Peptide
1	B	34	LEU	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3865	0	3759	51	0
1	B	3878	0	3763	58	0
2	C	39	0	34	10	0
2	D	39	0	34	13	0
3	A	10	0	10	4	0
3	B	10	0	10	6	0
4	A	30	0	0	1	0
4	B	30	0	0	1	0
5	A	14	0	11	0	0
5	B	14	0	12	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	369	0	0	7	0
7	B	372	0	0	12	0
All	All	8672	0	7633	119	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (119) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:19:ASN:HD21	2:D:1:NAG:C1	0.98	1.63
1:A:19:ASN:HD21	2:C:1:NAG:C1	0.97	1.54
1:B:19:ASN:ND2	2:D:1:NAG:C1	1.80	1.43
1:A:169:GLN:HG3	1:A:170:ARG:HG3	1.39	1.05
1:A:2:ARG:HG3	1:A:2:ARG:HH11	1.23	1.02
1:A:474:ASP:HB3	1:A:477:VAL:HG12	1.40	1.01
3:B:1501:FUC:C1	2:D:1:NAG:O3	2.10	0.99
1:A:474:ASP:HB3	1:A:477:VAL:CG1	1.93	0.97
1:B:474:ASP:HB3	1:B:477:VAL:CG1	1.97	0.95
1:B:95:ALA:HB1	1:B:406:ILE:HD12	1.51	0.92
1:A:95:ALA:HB1	1:A:406:ILE:HD12	1.56	0.87
1:A:19:ASN:HD21	2:C:1:NAG:C2	1.89	0.83
1:A:169:GLN:CG	1:A:170:ARG:HG3	2.09	0.82
1:B:474:ASP:HB3	1:B:477:VAL:HG12	1.60	0.80
1:B:19:ASN:HD21	2:D:1:NAG:C2	1.93	0.80
1:B:0:PHE:CB	7:B:2097:HOH:O	2.31	0.79
1:A:19:ASN:CG	2:C:1:NAG:C1	2.53	0.77
1:B:19:ASN:CG	2:D:1:NAG:C1	2.54	0.76
3:A:1502:FUC:H3	2:C:1:NAG:O3	1.87	0.74
1:A:474:ASP:CB	1:A:477:VAL:HG12	2.16	0.72
1:A:142:PHE:O	1:A:211:ARG:NH2	2.23	0.71
1:B:497:GLN:CG	7:B:2352:HOH:O	2.37	0.71
1:A:2:ARG:HG3	1:A:2:ARG:NH1	2.01	0.70
1:B:467:ASP:HB3	1:B:483:ILE:HD11	1.74	0.69
1:B:474:ASP:CB	1:B:477:VAL:HG12	2.21	0.69
1:A:7:LYS:HE3	1:A:9:PHE:CZ	2.29	0.67
1:A:26:PHE:CG	1:A:425:LYS:HE2	2.29	0.67
1:A:328:HIS:HD2	7:A:2259:HOH:O	1.78	0.67
1:A:151:GLU:HG3	7:A:2143:HOH:O	1.95	0.67
1:A:60:HIS:HD2	1:A:481:GLU:OE2	1.79	0.66
1:B:7:LYS:HE3	1:B:9:PHE:CZ	2.30	0.65
1:B:328:HIS:HD2	7:B:2259:HOH:O	1.80	0.64
1:B:474:ASP:CB	1:B:477:VAL:CG1	2.73	0.64
1:B:59:ASN:CB	7:B:2058:HOH:O	2.46	0.63
1:A:346:LYS:HB2	1:A:349:GLU:CD	2.20	0.63
1:A:474:ASP:CB	1:A:477:VAL:CG1	2.74	0.63
1:B:47:ARG:HD3	7:B:2046:HOH:O	1.98	0.62
3:A:1502:FUC:C1	2:C:1:NAG:O3	2.48	0.61
1:A:386:ASN:HB2	1:A:387:PRO:CD	2.30	0.61
1:B:142:PHE:O	1:B:211:ARG:NH2	2.34	0.60
1:B:395:ARG:NH1	7:B:2295:HOH:O	2.26	0.60
1:A:467:ASP:HB3	1:A:483:ILE:HD11	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:GLU:HA	7:B:2368:HOH:O	2.02	0.59
1:A:19:ASN:ND2	2:C:1:NAG:C2	2.58	0.58
3:A:1502:FUC:C3	2:C:1:NAG:O3	2.53	0.57
1:A:26:PHE:CD2	1:A:425:LYS:HE2	2.40	0.57
1:B:26:PHE:HZ	1:B:49:MET:HE2	1.71	0.54
1:B:474:ASP:CG	1:B:477:VAL:HG12	2.27	0.54
1:A:60:HIS:CD2	1:A:481:GLU:OE2	2.59	0.54
1:B:19:ASN:ND2	2:D:1:NAG:C2	2.62	0.53
1:A:406:ILE:HG22	7:A:2304:HOH:O	2.09	0.53
1:A:19:ASN:ND2	2:C:1:NAG:O5	2.32	0.52
1:A:300:GLU:CG	7:A:2235:HOH:O	2.56	0.52
1:B:95:ALA:HB1	1:B:406:ILE:CD1	2.32	0.52
1:A:318:ALA:HB1	1:A:323:THR:HG21	1.92	0.51
1:A:451:HIS:HD2	1:A:457:VAL:HG23	1.76	0.51
1:A:36:THR:HG22	7:A:2058:HOH:O	2.10	0.51
1:B:386:ASN:HB2	1:B:387:PRO:CD	2.40	0.51
1:B:450:MET:HE3	1:B:454:GLY:HA2	1.93	0.51
3:B:1501:FUC:H5	2:D:1:NAG:O3	2.11	0.50
1:B:66:LEU:HD11	1:B:473:LYS:HB2	1.94	0.50
1:A:252:THR:HB	1:A:253:PRO:HD2	1.95	0.48
1:B:47:ARG:CD	7:B:2046:HOH:O	2.58	0.48
1:B:463:ARG:HD3	7:B:2325:HOH:O	2.14	0.48
1:A:19:ASN:OD1	2:C:1:NAG:C1	2.62	0.48
1:B:98:PRO:N	1:B:99:PRO:CD	2.77	0.48
1:B:19:ASN:OD1	2:D:1:NAG:C1	2.62	0.47
1:A:446:ALA:HA	1:A:459:VAL:O	2.15	0.47
1:B:26:PHE:CZ	1:B:49:MET:HE2	2.49	0.47
1:B:427:ILE:HG22	1:B:427:ILE:O	2.13	0.47
1:B:169:GLN:CB	4:B:1507:SO4:O1	2.63	0.47
1:A:451:HIS:HD2	1:A:457:VAL:CG2	2.28	0.46
1:B:474:ASP:CG	1:B:477:VAL:CG1	2.84	0.46
1:B:497:GLN:CG	7:B:2330:HOH:O	2.63	0.46
1:A:44:ARG:HB3	4:A:1506:SO4:O3	2.16	0.46
1:A:395:ARG:HD3	7:A:2299:HOH:O	2.15	0.46
1:B:368:ILE:HG21	1:B:445:ASP:HB3	1.98	0.46
1:A:66:LEU:HD11	1:A:473:LYS:HB2	1.98	0.45
1:B:138:THR:HA	1:B:139:PRO:HD3	1.84	0.45
1:B:165:LEU:CD2	1:B:172:VAL:HB	2.47	0.45
1:B:286:LEU:C	1:B:286:LEU:HD12	2.36	0.45
1:B:159:PRO:O	1:B:163:ARG:HG3	2.17	0.45
1:B:211:ARG:HD2	7:B:2169:HOH:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:ALA:O	1:A:223:HIS:HD2	2.00	0.45
1:B:176:ALA:HB2	1:B:227:PHE:CE2	2.52	0.45
3:B:1501:FUC:C1	2:D:1:NAG:C3	2.92	0.44
1:B:243:GLY:O	1:B:244:TYR:C	2.55	0.43
1:A:386:ASN:HB2	1:A:387:PRO:HD3	1.98	0.43
3:B:1501:FUC:H3	2:D:1:NAG:O3	2.18	0.43
1:A:98:PRO:N	1:A:99:PRO:CD	2.81	0.43
1:B:219:ALA:O	1:B:223:HIS:HD2	2.02	0.43
1:A:451:HIS:CD2	1:A:457:VAL:CG2	3.01	0.42
1:A:95:ALA:HB1	1:A:406:ILE:CD1	2.40	0.42
1:A:427:ILE:HG22	1:A:427:ILE:O	2.19	0.42
1:A:26:PHE:HZ	1:A:49:MET:HE2	1.85	0.42
1:B:79:LYS:HA	1:B:79:LYS:HD2	1.86	0.42
3:A:1502:FUC:H5	2:C:1:NAG:O3	2.19	0.42
1:B:28:PRO:HA	1:B:29:PRO:HD3	1.89	0.42
1:B:93:ILE:O	1:B:101:GLN:HG2	2.19	0.42
1:B:395:ARG:NH1	7:B:2294:HOH:O	2.36	0.42
1:B:312:TRP:CD1	1:B:312:TRP:C	2.93	0.42
1:A:176:ALA:HB3	1:A:230:VAL:HG12	2.02	0.41
1:B:26:PHE:HZ	1:B:49:MET:SD	2.43	0.41
1:A:60:HIS:HE1	7:A:2070:HOH:O	2.03	0.41
1:A:165:LEU:CD2	1:A:172:VAL:HB	2.51	0.41
1:B:49:MET:HG3	1:B:418:TYR:HD2	1.85	0.41
1:B:104:LEU:C	1:B:104:LEU:HD23	2.40	0.41
3:B:1501:FUC:C3	2:D:1:NAG:O3	2.69	0.41
1:B:253:PRO:HB3	1:B:291:TRP:CD2	2.55	0.41
1:A:201:PRO:HA	1:A:206:HIS:CG	2.55	0.41
1:B:160:LEU:HA	1:B:160:LEU:HD23	1.88	0.41
3:B:1501:FUC:C2	2:D:1:NAG:O3	2.67	0.41
1:A:138:THR:HA	1:A:139:PRO:HD3	1.88	0.41
1:B:47:ARG:HD2	1:B:50:GLU:OE1	2.21	0.41
1:B:252:THR:HB	1:B:253:PRO:HD2	2.03	0.41
1:B:26:PHE:HZ	1:B:49:MET:CE	2.33	0.40
1:B:19:ASN:ND2	2:D:1:NAG:O5	2.44	0.40
1:A:286:LEU:HD12	1:A:286:LEU:C	2.42	0.40
1:A:462:ASN:HB2	1:A:484:SER:OG	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	489/505 (97%)	464 (95%)	22 (4%)	3 (1%)	25	31
1	B	491/505 (97%)	468 (95%)	22 (4%)	1 (0%)	47	58
All	All	980/1010 (97%)	932 (95%)	44 (4%)	4 (0%)	34	42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	ALA
1	A	281	LEU
1	B	281	LEU
1	A	124	ALA

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

6 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	2,1	14,14,15	0.72	0	17,19,21	1.46	3 (17%)
2	NAG	C	2	2	14,14,15	0.52	0	17,19,21	1.72	3 (17%)
2	BMA	C	3	2	11,11,12	0.71	0	15,15,17	1.54	3 (20%)
2	NAG	D	1	2	14,14,15	0.59	0	17,19,21	1.25	3 (17%)
2	NAG	D	2	2	14,14,15	0.62	0	17,19,21	1.92	3 (17%)
2	BMA	D	3	2	11,11,12	0.65	0	15,15,17	1.52	3 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	3/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	NAG	D	1	2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	3/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C4-C3-C2	-5.61	102.79	111.02
2	C	2	NAG	C4-C3-C2	-5.36	103.17	111.02
2	D	3	BMA	C1-C2-C3	3.58	114.06	109.67
2	D	2	NAG	O5-C1-C2	-3.50	105.76	111.29
2	C	2	NAG	O5-C1-C2	-3.35	106.00	111.29
2	C	3	BMA	C1-C2-C3	3.18	113.58	109.67
2	C	1	NAG	C1-O5-C5	-2.97	108.17	112.19
2	D	3	BMA	O5-C1-C2	2.81	115.11	110.77
2	C	3	BMA	O5-C1-C2	2.70	114.94	110.77
2	D	1	NAG	C2-N2-C7	-2.55	119.28	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	NAG	C2-N2-C7	-2.52	119.31	122.90
2	C	3	BMA	O5-C5-C6	2.44	111.03	107.20
2	D	1	NAG	O5-C5-C6	2.39	110.94	107.20
2	C	1	NAG	C4-C3-C2	-2.29	107.66	111.02
2	C	2	NAG	C1-C2-N2	2.05	114.00	110.49
2	D	3	BMA	C2-C3-C4	2.05	114.45	110.89
2	D	2	NAG	C1-C2-N2	2.04	113.98	110.49
2	D	1	NAG	O7-C7-C8	-2.02	118.30	122.06

There are no chirality outliers.

All (6) torsion outliers are listed below:

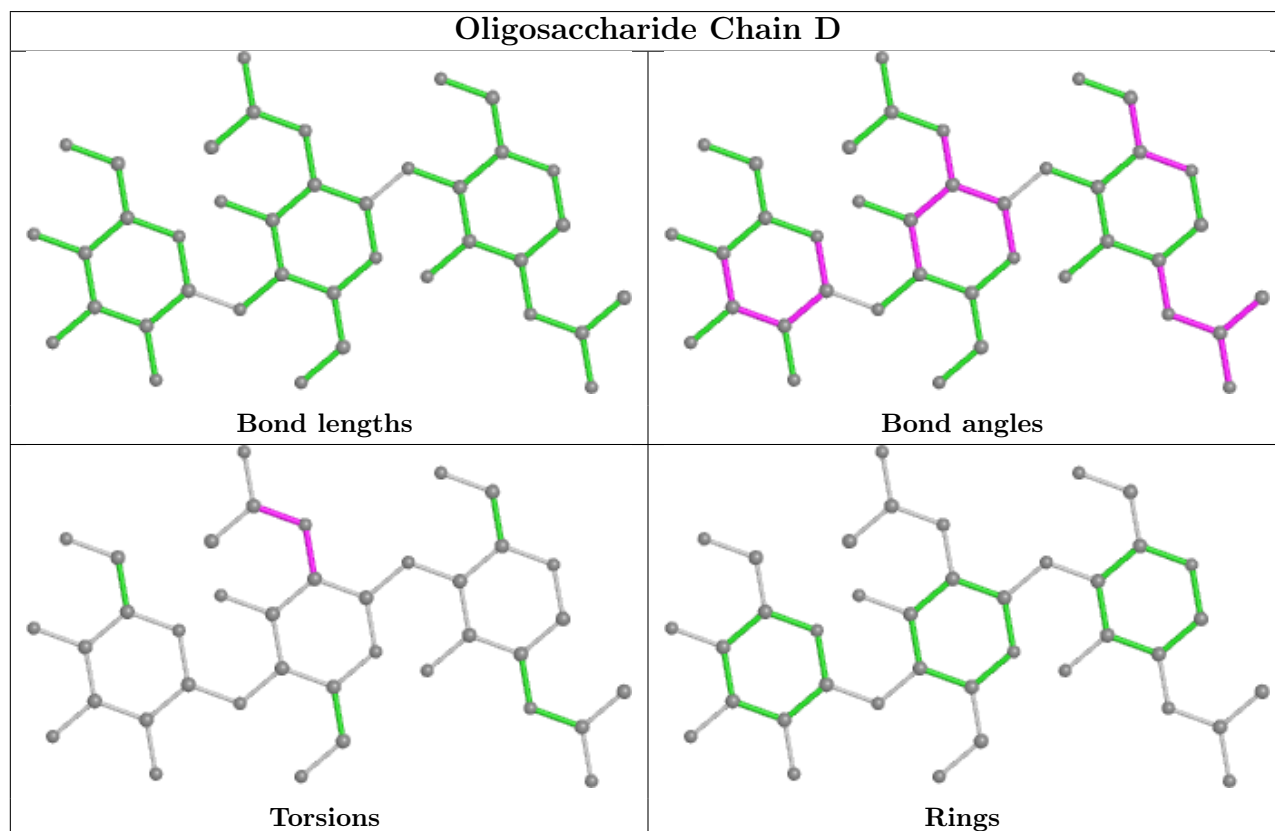
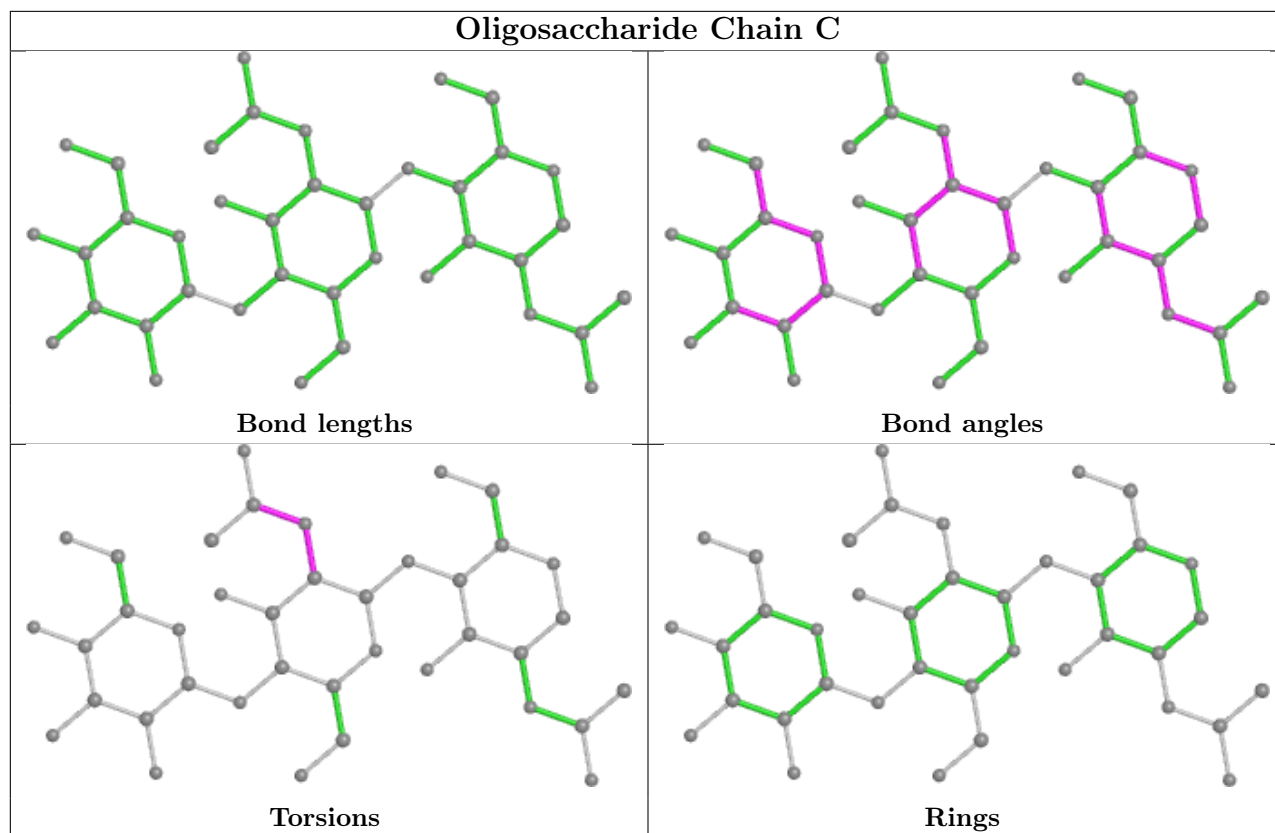
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	C	2	NAG	C1-C2-N2-C7
2	D	2	NAG	C1-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	NAG	13	0
2	C	1	NAG	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	A	1505	-	4,4,4	0.20	0	6,6,6	0.65	0
3	FUC	A	1502	-	10,10,11	0.81	0	14,14,16	1.33	2 (14%)
4	SO4	B	1506	-	4,4,4	0.17	0	6,6,6	0.28	0
4	SO4	B	1502	-	4,4,4	0.17	0	6,6,6	0.50	0
4	SO4	A	1504	-	4,4,4	0.22	0	6,6,6	0.34	0
4	SO4	B	1505	-	4,4,4	0.22	0	6,6,6	0.37	0
4	SO4	B	1507	-	4,4,4	0.20	0	6,6,6	0.54	0
5	MT5	A	1509	-	12,15,23	1.49	2 (16%)	11,23,31	2.68	4 (36%)
5	MT5	B	1508	-	12,15,23	1.14	1 (8%)	11,23,31	2.74	4 (36%)
4	SO4	A	1508	-	4,4,4	0.19	0	6,6,6	0.57	0
4	SO4	A	1506	-	4,4,4	0.21	0	6,6,6	0.54	0
4	SO4	A	1503	-	4,4,4	0.21	0	6,6,6	0.40	0
4	SO4	B	1504	-	4,4,4	0.28	0	6,6,6	0.48	0
3	FUC	B	1501	-	10,10,11	0.80	0	14,14,16	1.41	1 (7%)
4	SO4	A	1507	-	4,4,4	0.20	0	6,6,6	0.55	0
4	SO4	B	1503	-	4,4,4	0.16	0	6,6,6	0.26	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MT5	B	1508	-	-	-	0/2/2/2
3	FUC	B	1501	-	-	-	0/1/1/1
5	MT5	A	1509	-	-	-	0/2/2/2
3	FUC	A	1502	-	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1509	MT5	O16-C15	-3.37	1.36	1.40
5	B	1508	MT5	C13-N14	-2.71	1.43	1.47
5	A	1509	MT5	C21-C13	-2.70	1.47	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1508	MT5	O16-C15-N14	5.21	120.19	111.90
5	A	1509	MT5	O16-C15-N14	5.14	120.08	111.90
5	B	1508	MT5	C19-C21-C13	-4.66	103.50	111.37
5	B	1508	MT5	O18-C17-C15	4.52	117.97	109.19
5	A	1509	MT5	C19-C17-C15	4.00	115.29	109.05
5	A	1509	MT5	C19-C21-C13	-3.77	105.00	111.37
5	A	1509	MT5	O18-C17-C15	3.43	115.85	109.19
3	A	1502	FUC	C1-C2-C3	2.88	113.20	109.67
5	B	1508	MT5	C19-C17-C15	2.77	113.37	109.05
3	B	1501	FUC	O2-C2-C3	-2.22	105.70	110.14
3	A	1502	FUC	O5-C5-C4	2.09	113.26	109.52

There are no chirality outliers.

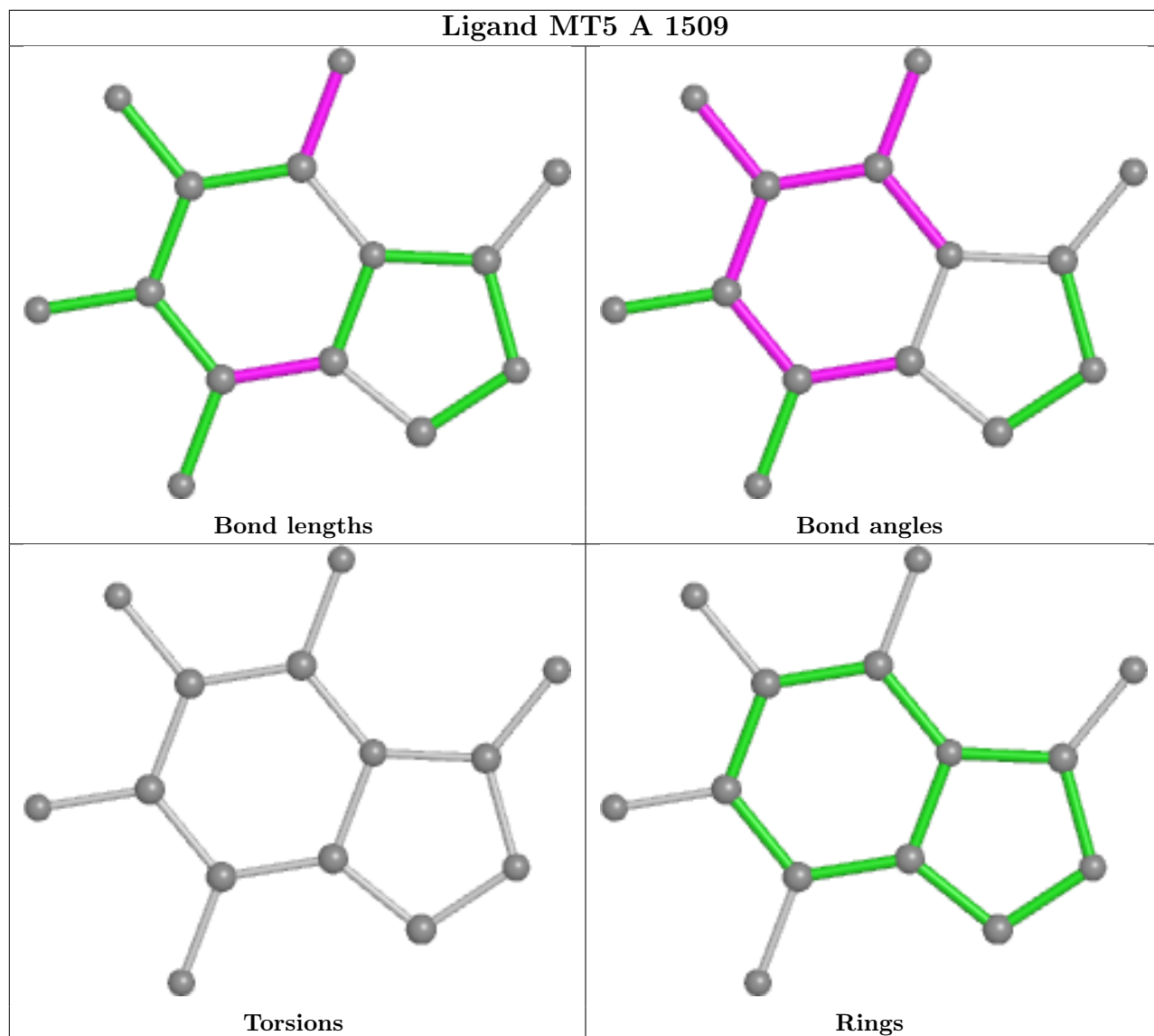
There are no torsion outliers.

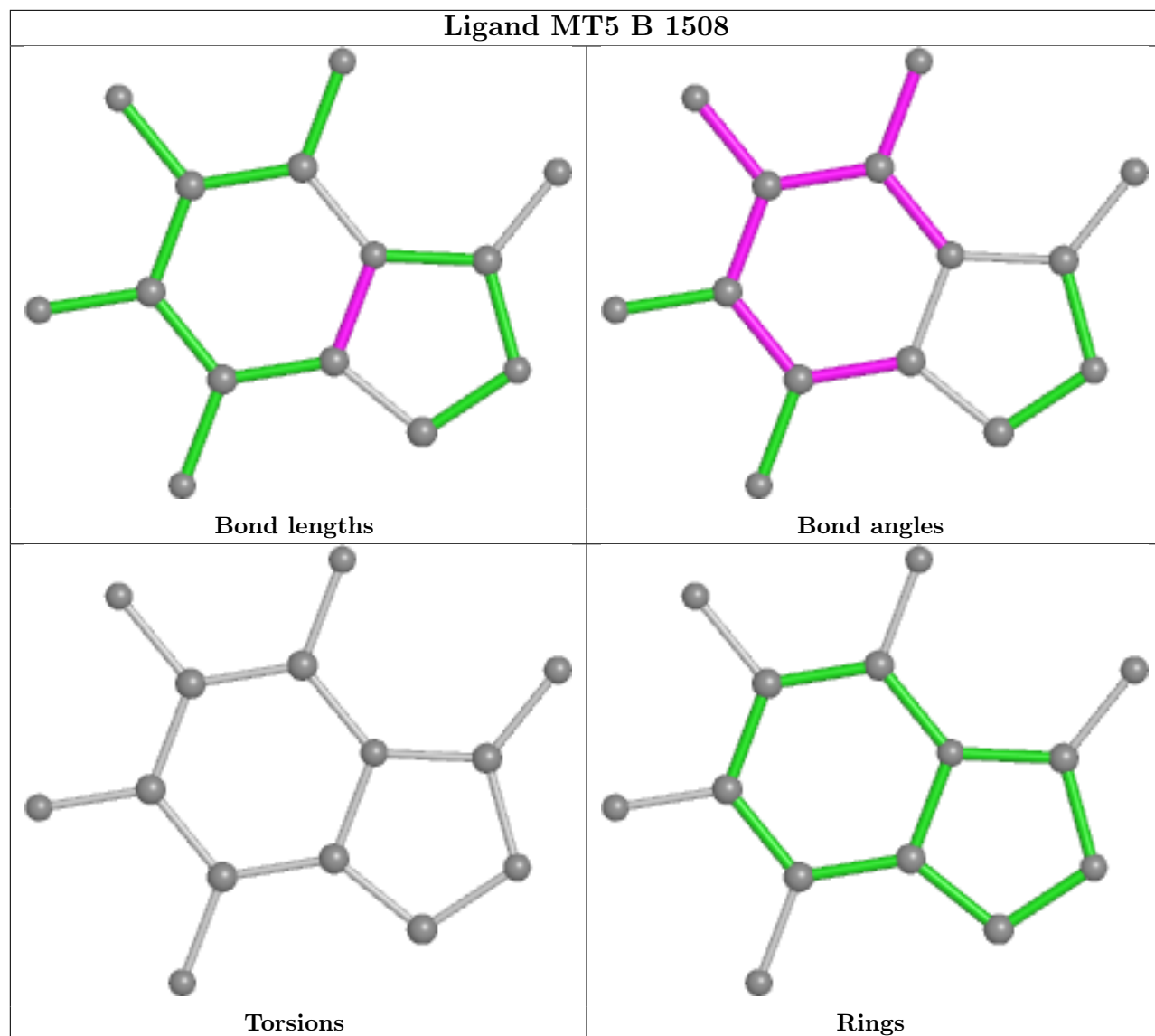
There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1502	FUC	4	0
4	B	1507	SO4	1	0
4	A	1506	SO4	1	0
3	B	1501	FUC	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.